



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gregory Plowman
Bahija Jallal
- (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
PTP RELATED DISORDERS
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Brobeck, Phleger & Harrison LLP
(B) STREET: 12390 El Camino Real
(C) CITY: San Diego
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 92130-2081
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/095,478
(B) FILING DATE: June 10, 1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/049,756
(B) FILING DATE: June 11, 1997

(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 235/054

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	1785 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

B1
B2

GGTTATGTCT GACTCACTGC ACTGGAGTTT GGCAAAAGCA TCTCAGAAGT GGTTGTGCTT	60
TTTTGAATGA AATGATCAAT GGAGTGCTCC AGTTGTATGC TGGCCTCTGG ATACTAACTA	120
GACCTGCCTG ACTCCAGGAA CTAAGGCTCA GTATCTGCAG AAGCTTTTG CCCATCTCAT	180
TCCGGCTATG GGGACAACAT GTCTTCACCC AGGAAGGTTA GAGGAAAAAC TGGAAGAGAT	240
AATGATGAAG AGGAGGGTAA TTCAGGTAAC CTGAATCTCC GCAACTCTT GCCTTCATCG	300
AGTCAGAAAA TGACGCCCTAC GAAGCCGATT TTTGGAATA AAATGAATTC AGAGAATGTA	360
AAACCCCTCCC ATCACCTGTC ATTCTCAGAT AAGTATGAGC TTGTTTACCC AGAGCCTTTG	420
GAAAGTGACA CTGATGAGAC TGTGTGGGAT GTCAGTGACC GGTCTCTCAG AAACAGGTGG	480
AACAGTATGG ATTCAAGAGAC TGCAGGGCCG TCAAAGACTG TCTCCCCAGT GCTTCTGGT	540
AGTAGTAGGC TCTCAAAGGA CACTGAAACA TCTGTCTCTG AAAAGGAGCT AACTCAGTTG	600
GCTCAGATTC GACCATTAAT ATTCAACAGT TCTGCACGGT CTGCTATGCG GGATTGTTG	660
AACACGCTTC AGAAAAAAAGA AGAACATTGAT ATCATCCGTG AGTTTTGGA GTTAGAACAA	720
ATGACTCTGC CTGATGACTT CAATTCTGGG AATACACTAC AGAACAGAGA TAAGAACAGA	780
TACCGAGATA TTCTTCCATA TGATTCAACA CGTGTTCCTC TTGGAAAAAA CAAGGACTAC	840
ATCAACGCTA GTTATATTAG AATAGTAAAT CATGAGAAG AGTATTTTTA TATTGCCACT	900
CAAGGACCAT TGCCAGAAC TATAGAAGAC TTTTGGCAAA TGGTTCTGGA AAATAATTGT	960
AATGTTATTG CTATGATAAC CAGAGAGATA GAATGTGGAG TTATCAAGTG TTACAGTTAC	1020
TGGCCCATTCT CTCTGAAGGA GCCTTTGGAA TTCGAACACT TTAGTGTCTT TCTGGAGACC	1080
TTTCATGTAA CTCAATATTT CACCGTTCGA GTATTTCAGA TTGTGAAGAA GTCCACAGGA	1140
AAGAGCCAAT GTGTAAAACA CTTGCAGTTC ACCAAGTGGC CAGACCATGG CACTCCTGCC	1200
TCAGCAGATT TTTTCATAAA ATATGTCGGT TATGTGAGGA AGAGCCACAT TACAGGACCC	1260
CTCCTTGTTC ACTGCAGTGC TGGTGTAGGC CGAACAGGGG TGTTCATATG TGTGGATGTT	1320
GTGTTCTCTG CCATCGAGAA GAACTACTCT TTTGACATTA TGAACATAGT GACCCAGATG	1380
AGAAAGCAGC GCTGTGGCAT GATTCAAACC AAGGAGCAGT ACCAGTTTG TTATGAAATT	1440
GTGCTTGAAG TTCTTCAGAA CCTTCTGGCT TTGTATTAAG AGAGACTTCT GCGCCTGTCC	1500
CTCGAGGTTA CCGAGCAGCT TGGAGCCTGA GCCGTGCTGA AGCGTCTGCG GGCGTGCAG	1560
TCTGCCTTCT GATTTTCTC TCTGAAAGTC CCTGAAGGTA GCAACTACTGG GCACAGAGTG	1620
AACTGTTTC CACTGATCTT TCTGAACAAAG AGCAAAATAC CCTCCATGCC TTCTACGGAA	1680
ACGGAAGTTG CATGAAACAA CCTCCGCTTG GCTGTCTGGT TTGTGGTATT ACAGAGCTTA	1740
ATAAAAGACT TAGATGTGAA AAAAAAAAAA AAAAAAAA AAAAA	1785

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGTTATGTCT GACTCACTGC ACTGGAGTTT GGCAAAAGCA TCTCAGAAGT GGTTGTGCTT	60
TTTTGAATGA AATGATCAAT GGAGTGCTCC AGTTGTATGC TGGCCTCTGG ATACTAACTA	120
GACCTGCCTG ACTCCAGGAA CTAAGGCTCA GTATCTGCAG AAGCTTTTG CCCATCTCAT	180
TCCGGCTATG GGGACAAACAT GTCTTCACCC AGGAAGGTTA GAGGAAAAAC TGGAAGAGAT	240
AATGATGAAG AGGAGGGTAA TTCAGGTAAC CTGAATCTCC GCAACTCTT GCCTTCATCG	300
AGTCAGAAAA TGACGCCAAC GAAGCCGGTA CAAAATAAAA ATCTCATGAA GTATGAAGAA	360
CACTTAGATA TATTGATGGT GTTTTATTG ATAAAAAACCA TATGGTATAA TGTCTTCAAA	420
TTATGGAAAG GCAAGCTTAT TTTTGGGAAT AAAATGAATT CAGAGAATGT AAAACCCCTCC	480
CATCACCTGT CATTCTCAGA TAAGTATGAG CTTGTTTACCC CAGAGCCTT GGAAAGTGC	540
ACTGATGAGA CTGTGTGGGA TGTCAGTGC CGGTCTCTCA GAAACAGGTG GAACAGTATG	600
GATTCAAGAGA CTGCAGGGCC GTCAAAGACT GTCTCCCCAG TGCTTCTGG TAGTAGTAGG	660
CTCTCAAAGG ACACGAAAC ATCTGTCTT GAAAAGGAGC TAACTCAGTT GGCTCAGATT	720
CGACCAATTAA TATTCAACAG TTCTGCACGG TCTGCTATGC GGGATTGTTT GAACACGCTT	780
CAGAAAAAAAG AAGAACTTGA TATCATCCGT GAGTTTTGG AGTTAGAACAA ATGACTCTG	840
CCTGATGACT TCAATTCTGG GAATACACTA CAGAACAGAG ATAAGAACAG ATACCGAGAT	900
ATTCTTCCAT ATGATTCAAC ACGTGTTCTT CTTGGAAAAA ACAAGGACTA CATCAACGCT	960
AGTTATATTA GAATAGTAA TCATGAAGAA GAGTATTTT ATATTGCCAC TCAAGGACCA	1020
TTGCCAGAAA CTATAGAAGA CTTTTGGCAA ATGGTTCTGG AAAATAATTG TAATGTTATT	1080
GCTATGATAA CCAGAGAGAT AGAATGTGGA GTTATCAAGT GTTACAGTTA CTGGCCCATT	1140
TCTCTGAAGG AGCCTTGGGA ATTGAAACAC TTTAGTGTCT TTCTGGAGAC CTTTCATGTA	1200
ACTCAATATT TCACCGTTCG AGTATTTCAAG ATTGTGAAGA AGTCCACAGG AAAGAGCCAA	1260
TGTGTAAAAC ACTTGAGTT CACCAAGTGG CCAGACCATG GCACTCCTGC CTCAGCAGAT	1320
TTTTTCATAA AATATGTCCG TTATGTGAGG AAGAGCCACA TTACAGGACC CCTCCTTGTT	1380
CACTGCAGTG CTGGTGTAGG CCGAACAGGG GTGTTCATAT GTGTGGATGT TGTGTTCTCT	1440
GCCATCGAGA AGAACTACTC TTTGACATT ATGAACATAG TGACCCAGAT GAGAAAGCAG	1500
CGCTGTGGCA TGATTCAAAC CAAGGAGCAG TACCAGTTT GTTATGAAAT TGTGCTTGAA	1560
GTTCTTCAGA ACCTTCTGGC TTTGTATTAA GAGAGACTTC TGCGCCTGTC CCTCGAGGTT	1620
ACCGAGCAGC TTGGAGCCTG AGCCGTGCTG AAGCGTCTGC GGGCCGTGCA GTCTGCCTTC	1680
TGATTTTCT CTCTGAAAGT CCCTGAGGT AGCACTACTG GGCACAGAGT GAACTGTTTC	1740
CACTTGATCT TTCTGAACAA GAGCAAATAA CCCTCCATGC CTTCTACGGA AACGGAAGTT	1800
GCATGAAACA ACCTCCGCTT GGCTGTCTGG TTTGTGGTAT TACAGAGCTT AATAAAAGAC	1860
TTAGATGTGA AAAAAAAAAA AAAAAAAAAA AAAAAAA	1896

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTTATGTCT GACTCACTGC ACTGGAGTTT GGCAAAAGCA TCTCAGAAGT GGTTGTGCTT	60
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TTTGAAATGA AATGATCAAT GGAGTGCTCC AGTTGTATGC TGGCCTCTGG ATACTAACTA	120
GACCTGCCCTG ACTCCAGGAA CTAAGGCTCA GTATCTGCAG AAGCTTTTG CCCATCTCAT	180
TCCGGCTATG GGGACAACAT GTCTTCACCC AGGAAGGTTA GAGGAAAAAC TGGAAGAGAT	240
AATGATGAAG AGGAGGGTAA TTCAGGTAAC CTGAATCTCC GCAACTCTT GCCTTCATCG	300
AGTCAGAAAA TGACGCCCTAC GAAGCCGATT TTTGGGAATA AAATGAATTC AGAGAATGTA	360
AAACCCCTCCC ATCACCTGTC ATTCTCAGAT AAGTATGAGC TTGTTTACCC AGAGCCTTG	420
GAAAGTGCACA CTGATGAGAC TGTGTGGGAT GTCAGTGACC GGTCTCTCAG AAACAGGTGG	480
AACAGTATGG ATTCAAGAGAC TGCAAGGGCCG TCAAAGACTG TCTCCCCAGT GCTTTCTGGT	540
AGTAGTAGGC TCTCAAGGA CACTGAAACA TCTGTCTCTG AAAAGGAGCT AACTCAGTTG	600
GCTCAGATTC GACCATTAAAT ATTCAACAGT TCTGCACGGT CTGCTATGCG GGATTGTTG	660
AACACGCTTC AGAAAAAAAAGA AGAACATTGAT ATCATCCGTG AGTTTTGGA GTTAAACAA	720
ATGACTCTGC CTGATGACTT CAATTCTGGG AATACACTAC AGAACAGAGA TAAGAACAGA	780
TACCGAGATA TTCTTCCATA TGATTCAACA CGTGTTCCTC TTGGAAAAAA CAAGGACTAC	840
ATCAACGCTA GTTATATTAG AATAGTAAAT CATGAAGAAG AGTATTTTA TATTGCCACT	900
CAAGGACCAT TGCCAGAAC TATAGAAGAC TTTTGGCAAA TGTTCTGGA AAATAATTGT	960
AATGTTATTG CTATGATAAC CAGAGAGATA GAATGTGGAG TTATCAAGTG TTACAGTTAC	1020
TGGCCCATTCTCTGAAGGA GCCTTTGGAA TTCGAACACT TTAGTGTCTT TCTGGAGACC	1080
TTTCATGTAA CTCAATATTT CACCGTTCGA GTATTTCAGA TTGTGAAGAA GTCCACAGGA	1140
AAGAGCCAAT GTGTAAAACA CTTGCAGTTC ACCAAGTGGC CAGACCATGG CACTCCTGCC	1200
TCAGCAGATT TTTTCATAAA ATATGTCCGT TATGTGAGGA AGAGCCACAT TACAGGACCC	1260
CTCCTTGTTC ACTGCAGTGC TGGTGTAGGC CGAACAGGGG TGTTCATATG TGTGGATGTT	1320
GTGTTCTCTG CCATCGAGAA GAACTACTCT TTTGACATTA TGAACATAGT GACCCAGATG	1380
AGAAAGCAGC GCTGTGGCAT GATTCAAACCC AAGGTTACCG AGCAGCTTGG AGCCTGAGCC	1440
GTGCTGAAGC GTCTGGGGC CGTGCAGTCT GCCTCTGAT TTTTCTCTCT GAAAGTCCCT	1500
GAAGGTAGCA CTACTGGGCA CAGAGTGAAC TGTTCCACT TGATCTTCT GAACAAGAGC	1560
AAAATACCCCT CCATGCCCTTC TACGGAAACG GAAGTTGCAT GAAACAACCT CCGCTTGGCT	1620
GTCTGGTTTG TGGTATTACA GAGCTTAATA AAAGACTTAG ATGTAAAAAA AAAAAAAAAAA	1680
AAAAAAAAAA AA	1692

b1 w/
(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAAAATAATT GTAATGTTAT TGCTATGATA ACCAGAGAGA TAGAAGGTGG AGTTATCAAG	60
TGTTGCAGTT ACTGGCCCGT TTCTCTGAAG GAGCCTTTGG AATTCAAACA CTTTCATGTC	120
CTTCTGGAGA ACTTTCAAGAT AACTCAGTAT TTTGTCATCC GAATATTCA AATTGTGAAG	180
AAGTCCACAG GAAAGAGTCA CTCTGTAAAA CACTTGAGT TCATCAAATG GCCAGACCAT	240
GGCACTCCTG CCTCAGTAGA TTTTTTCATC AAATATGTCC GTTATGTGAG GAAGAGCCAC	300
ATTACAGGAC CCCTCCTTGT	320

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
 20 25 30

Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Ile Phe Gly Asn Lys
 35 40 45

Met Asn Ser Glu Asn Val Lys Pro Ser His His Leu Ser Phe Ser Asp
 50 55 60

Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu Ser Asp Thr Asp Glu
 65 70 75 80

Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser
 85 90 95

Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu
 100 105 110

B1
 Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu
 115 120 125

Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser
 130 135 140

Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys
 145 150 155 160

Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr
 165 170 175

Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys
 180 185 190

Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu
 195 200 205

Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn
 210 215 220

His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu
 225 230 235 240

Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val
 245 250 255

Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr

260

265

270

Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe
 275 280 285

Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg
 290 295 300

Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys
 305 310 315 320

His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala
 325 330 335

Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr
 340 345 350

Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val
 355 360 365

Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser
 370 375 380

Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly
 385 390 395 400

Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys Tyr Glu Ile Val Leu
 405 410 415

Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr
 420 425

B1
 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
 20 25 30

Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Val Gln Asn Lys Asn
 35 40 45

Leu Met Lys Tyr Glu Glu His Leu Asp Ile Leu Met Val Phe Leu Leu

50	55	60	
Ile Lys Thr Ile Trp Tyr Asn Val Phe Lys Leu Trp Lys Gly Lys Leu			
65	70	75	80
Ile Phe Gly Asn Lys Met Asn Ser Glu Asn Val Lys Pro Ser His His			
85	90	95	
Leu Ser Phe Ser Asp Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu			
100	105	110	
Ser Asp Thr Asp Glu Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg			
115	120	125	
Asn Arg Trp Asn Ser Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr			
130	135	140	
Val Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu			
145	150	155	160
Thr Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro			
165	170	175	
Leu Ile Phe Asn Ser Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn			
180	185	190	
Thr Leu Gln Lys Lys Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu			
195	200	205	
Leu Glu Gln Met Thr Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu			
210	215	220	
Gln Asn Arg Asp Lys Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser			
225	230	235	240
Thr Arg Val Pro Leu Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr			
245	250	255	
Ile Arg Ile Val Asn His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln			
260	265	270	
Gly Pro Leu Pro Glu Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu			
275	280	285	
Asn Asn Cys Asn Val Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly			
290	295	300	
Val Ile Lys Cys Tyr Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu			
305	310	315	320
Glu Phe Glu His Phe Ser Val Phe Leu Glu Thr Phe His Val Thr Gln			
325	330	335	
Tyr Phe Thr Val Arg Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys			
340	345	350	
Ser Gln Cys Val Lys His Leu Gln Phe Thr Lys Trp Pro Asp His Gly			

355	360	365
Thr Pro Ala Ser Ala Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg		
370	375	380
Lys Ser His Ile Thr Gly Pro Leu Leu Val His Cys Ser Ala Gly Val		
385	390	395
Gly Arg Thr Gly Val Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile		
405	410	415
Glu Lys Asn Tyr Ser Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg		
420	425	430
Lys Gln Arg Cys Gly Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys		
435	440	445
Tyr Glu Ile Val Leu Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr		
450	455	460

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

*B
w/k*

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp		
1	5	10
		15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro		
20	25	30

Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Ile Phe Gly Asn Lys		
35	40	45

Met Asn Ser Glu Asn Val Lys Pro Ser His His Leu Ser Phe Ser Asp		
50	55	60

Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu Ser Asp Thr Asp Glu		
65	70	75
		80

Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser		
85	90	95

Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu		
100	105	110

Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu

115	120	125
Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser		
130	135	140
Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys		
145	150	155
Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr		
165	170	175
Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys		
180	185	190
Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu		
195	200	205
Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn		
210	215	220
His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu		
225	230	235
Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val		
245	250	255
Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr		
260	265	270
Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe		
275	280	285
Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg		
290	295	300
Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys		
305	310	315
His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala		
325	330	335
Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr		
340	345	350
Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val		
355	360	365
Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser		
370	375	380
Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly		
385	390	395
Met Ile Gln Thr Lys		
	405	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Phe Trp Gly Met Met Trp Glu Asn Asn Cys Asn Val Ile Ala Met
 1 5 10 15

Ile Thr Arg Glu Ile Glu Gly Gly Val Ile Lys Cys Cys Ser Tyr Trp
 20 25 30

Pro Val Ser Leu Lys Glu Pro Leu Glu Phe Lys His Phe His Val Leu
 35 40 45

Leu Glu Asn Phe Gln Ile Thr Gln Tyr Phe Val Ile Arg Ile Phe Gln
 50 55 60

Ile Val Lys Lys Ser Thr Gly Lys Ser His Ser Val Lys His Leu Gln
 65 70 75 80

Phe Ile Lys Trp Pro Asp His Gly Thr Pro Ala Ser Val Asp Phe Phe
 85 90 95

Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr Gly Pro Leu
 100 105 110

Leu Val His Cys Thr Ala Gly Val Gly Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "Y" stands for C or T.

The letter "V" stands for A, C or G.

The letter "R" stands for A or G.

The letter "N" stands for A, C, G

or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAYTTYTGGV RNATGRTNTG GGA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: The letter "S" stands for C or G.
The letter "Y" stands for C or T.
The letter "N" stands for A, C, G
or T.
The letter "W" stands for A or T.
The letter "R" stands for A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

B1
Bw/
CGGCCSAYNC CNGCNSWRCA RTG

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: "Xaa" in positions 4 and 6 stand for an unspecified amino acid.
"Xaa" in position 8 stands for either Glu or Asp.

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Phe Trp Xaa Met Xaa Trp Xaa

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: "Xaa" in positions 3 and 6 stand for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

His Cys Xaa Ala Gly Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

B1
BwV
CACCCTTCGA GTATTCAGA TTGTGAAGAA GTCC

34

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACTTCTTC ACAATCTGAA ATACTCGAAC GGTG

34

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGTTATGTG AGGAAGAGCC ACATTACAGG ACC

33

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

33

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CACC GTTCGA GTATTCAGA TTGTGAAGAA GTCC

34

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

His Cys Ser Ala Gly
1 5

B1
WJ

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
 1 5 10 15

Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn
 20 25

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr
 1 5 10 15

Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile
 20 25

b/w (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser Met Asp
 1 5 10 15

Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val
 20 25

110